

*re-run***RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number:

10/540,494

Source:

pc

Date Processed by STIC:

*7/11/05****ENTERED***

re-run

P6

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/540,494

DATE: 04/10/2006

TIME: 12:14:37

Input Set : N:\Crf4\Refhold\10_folder\J540494.raw

Output Set: N:\CRF4\04102006\J540494.raw

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1 <110> APPLICANT: Takeda Pharmaceutical Company Limited
2 <120> TITLE OF INVENTION: Metastin Derivatives And Its Use
3 <130> FILE REFERENCE: G05-0018
4 <140> CURRENT APPLICATION NUMBER: US/10/540,494
5 <141> CURRENT FILING DATE: 2005-06-23
6 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/016978
7 <151> PRIOR FILING DATE: 2003-12-26
8 <150> PRIOR APPLICATION NUMBER: JP 2002-377179
9 <151> PRIOR FILING DATE: 2002-12-26
10 <160> NUMBER OF SEQ ID NOS: 22
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 54
14 <212> TYPE: PRT
15 <213> ORGANISM: Homo sapiens
16 <400> SEQUENCE: 1
17   Gly Thr Ser Leu Ser Pro Pro Pro Glu Ser Ser Gly Ser Arg Gln Gln
18       1             5             10             15
19   Pro Gly Leu Ser Ala Pro His Ser Arg Gln Ile Pro Ala Pro Gln Gly
20               20             25             30
21   Ala Val Leu Val Gln Arg Glu Lys Asp Leu Pro Asn Tyr Asn Trp Asn
22               35             40             45
23   Ser Phe Gly Leu Arg Phe
24       50
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 162
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 2
31   ggtacttctc tgtctccgcc gccggaatct tctggttctc gtcagcagcc gggctctgtct      60
32   gccccgcact ctgctcagat cccggtccg caggggtgctg ttctgggttca gcgtgaaaaa      120
33   gacctgccga actacaactg gaactctttc ggtctgcggt tc                        162
35 <210> SEQ ID NO: 3
36 <211> LENGTH: 152
37 <212> TYPE: PRT
38 <213> ORGANISM: Mus musculus
39 <400> SEQUENCE: 3
40   Met Tyr Leu Arg Phe Gly Val Asp Val Cys Ser Leu Ser Pro Trp Lys
41               5             10             15
42   Glu Thr Val Asp Leu Pro Leu Pro Pro Arg Met Ile Ser Met Ala Ser
43               20             25             30
44   Trp Gln Leu Leu Leu Leu Cys Val Ala Thr Tyr Gly Glu Pro Leu
45               35             40             45
46   Ala Lys Val Ala Pro Gly Ser Thr Gly Gln Gln Ser Gly Pro Gln Glu
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47          50          55          60
48  Leu Val Asn Ala Trp Glu Lys Glu Ser Arg Tyr Ala Glu Ser Lys Pro
49          65          70          75          80
50  Gly Ser Ala Gly Leu Arg Ala Arg Arg Ser Ser Pro Cys Pro Pro Val
51          85          90          95
52  Glu Gly Pro Ala Gly Arg Gln Arg Pro Leu Cys Ala Ser Arg Ser Arg
53          100          105          110
54  Leu Ile Pro Ala Pro Arg Gly Ala Val Leu Val Gln Arg Glu Lys Asp
55          115          120          125
56  Leu Ser Thr Tyr Asn Trp Asn Ser Phe Gly Leu Arg Tyr Gly Arg Arg
57          130          135          140
58  Gln Ala Ala Arg Ala Ala Arg Gly
59          145          150
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 456
63 <212> TYPE: DNA
64 <213> ORGANISM: Mus musculus
65 <400> SEQUENCE: 4
66  atgtatctga gatttggcgt tgatgtctgc agcctgagtc cctggaagga gactgtagac 60
67  ctgccccttc ctcccagaat gatctcaatg gcttcttggc agctgctgct tctctctgt 120
68  gtcgccacct atggggagcc gctggcaaaa gtgaagcctg gatccacagg ccagcagtc 180
69  ggaccccagg aactcggtta tgcctgggaa aaggaatcgc ggtatgcaga gagcaagcct 240
70  gggctctgca ggctgcgcgc tcgtaggctc tcgccatgcc cgcgggttga gggccccgcg 300
71  gggcgccagc ggcccctgtg tgcctcccgc agtcgcctga tccctgcgcc ccgcggagcg 360
72  gtgctggtgc agcgggagaa ggacctgtcc acctacaact ggaactcctt cggcctgcgc 420
73  tacggcagga ggcaggcgcc gcgggcagca cggggc 456
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 156
77 <212> TYPE: PRT
78 <213> ORGANISM: Mus musculus
79 <400> SEQUENCE: 5
80  Met Tyr Leu Arg Phe Gly Val Asp Val Cys Ser Leu Ser Pro Trp Lys
81          5          10          15
82  Glu Thr Val Asp Leu Pro Leu Pro Pro Arg Met Ile Ser Met Ala Ser
83          20          25          30
84  Trp Gln Leu Leu Leu Leu Cys Val Ala Thr Tyr Gly Glu Pro Leu
85          35          40          45
86  Ala Lys Val Ala Pro Leu Val Lys Pro Gly Ser Thr Gly Gln Gln Ser
87          50          55          60
88  Gly Pro Gln Glu Leu Val Asn Ala Trp Glu Lys Glu Ser Arg Tyr Ala
89          65          70          75          80
90  Glu Ser Lys Pro Gly Ser Ala Gly Leu Arg Ala Arg Arg Ser Ser Pro
91          85          90          95
92  Cys Pro Pro Val Glu Gly Pro Ala Gly Arg Gln Arg Pro Leu Cys Ala
93          100          105          110
94  Ser Arg Ser Arg Leu Ile Pro Ala Pro Arg Gly Ala Val Leu Val Gln
95          115          120          125
96  Arg Glu Lys Asp Leu Ser Thr Tyr Asn Trp Asn Ser Phe Gly Leu Arg
97          130          135          140

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98      Tyr Gly Arg Arg Gln Ala Ala Arg Ala Ala Arg Gly
99      145                      150                      155
101 <210> SEQ ID NO: 6
102 <211> LENGTH: 468
103 <212> TYPE: DNA
104 <213> ORGANISM: Mus musculus
105 <400> SEQUENCE: 6
106      atgtatctga gatttggcgt tgatgtctgc agcctgagtc cctggaagga gactgtagac      60
107      ctgccccttc ctcccagaat gatctcaatg gcttcttggc agctgctgct tctcctctgt      120
108      gtcgccacct atggggagcc gctggcaaaa gtggcacctt tggatgaagcc tggatccaca      180
109      ggccagcagt cgggacccca ggaactcggt aatgcctggg aaaaggaatc gcggtatgca      240
110      gagagcaagc ctgggtctgc agggctgcgc gctcgtaggc cgtcgccatg ccgcgcggtt      300
111      gagggccccc cggggcgcca gcggccctcg tgtgcctccc gcagtcgctt gatccctgcg      360
112      ccccgcggaq cgggtgctgg gacgcgggaq aaggacctgt ccacctacaa ctggaactcc      420
113      ttccggcctgc gctacggcag gaggcaggcg gcgcgggcag cacggggc      468
115 <210> SEQ ID NO: 7
116 <211> LENGTH: 130
117 <212> TYPE: PRT
118 <213> ORGANISM: Rattus sp.
119 <400> SEQUENCE: 7
120      Met Thr Ser Leu Ala Ser Trp Gln Leu Leu Leu Leu Leu Cys Val Ala
121                      5                      10                      15
122      Ser Phe Gly Glu Pro Leu Ala Lys Met Ala Pro Val Val Asn Pro Glu
123                      20                      25                      30
124      Pro Thr Gly Gln Gln Ser Gly Pro Gln Glu Leu Val Asn Ala Trp Gln
125                      35                      40                      45
126      Lys Gly Pro Arg Tyr Ala Glu Ser Lys Pro Gly Ala Ala Gly Leu Arg
127                      50                      55                      60
128      Ala Arg Arg Thr Ser Pro Cys Pro Pro Val Glu Asn Pro Thr Gly His
129                      65                      70                      75                      80
130      Gln Arg Pro Pro Cys Ala Thr Arg Ser Arg Leu Ile Pro Ala Pro Arg
131                      85                      90                      95
132      Gly Ser Val Leu Val Gln Arg Glu Lys Asp Met Ser Ala Tyr Asn Trp
133                      100                     105                     110
134      Asn Ser Phe Gly Leu Arg Tyr Gly Arg Arg Gln Val Ala Arg Ala Ala
135                      115                     120                     125
136      Arg Gly
137                      130
139 <210> SEQ ID NO: 8
140 <211> LENGTH: 390
141 <212> TYPE: DNA
142 <213> ORGANISM: Rattus sp.
143 <400> SEQUENCE: 8
144      atgaacctgc tggcttcttg gcagctgctg cttctcctct gtgtggcctc ttttggggag      60
145      ccactggcaa aaatggcacc tgtggtgaac cctgaaccca caggccaaca gtccggagcc      120
146      caggaactcg ttaatgcctg gnaaaagggc ccgcggtatg cagagagcaa gcctggggct      180
147      gcaggactgc gcgctcgccg aacatcgcca tgcgcgcggg tggagaaccc cacggggcac      240
148      cagcgcccc cgtgtgccac ccgcagtcgc ctgataccctg cgcgccgcgg atcggtgctg      300
149      gtgcagcgcg agaaggacat gtcagcctac aactggaact cctttggcct gcgctacggc      360

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150      aggaggcagg tggcgcgggc ggcacggggc
152 <210> SEQ ID NO: 9
153 <211> LENGTH: 398
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
156 <400> SEQUENCE: 9
157      Met His Thr Val Ala Thr Ser Gly Pro Asn Ala Ser Trp Gly Ala Pro
158                      5                      10                      15
159      Ala Asn Ala Ser Gly Cys Pro Gly Cys Gly Ala Asn Ala Ser Asp Gly
160                      20                      25                      30
161      Pro Val Pro Ser Pro Arg Ala Val Asp Ala Trp Leu Val Pro Leu Phe
162                      35                      40                      45
163      Phe Ala Ala Leu Met Leu Leu Gly Leu Val Gly Asn Ser Leu Val Ile
164                      50                      55                      60
165      Tyr Val Ile Cys Arg His Lys Pro Met Arg Thr Val Thr Asn Phe Tyr
166                      65                      70                      75                      80
167      Ile Ala Asn Leu Ala Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val
168                      85                      90                      95
169      Pro Phe Thr Ala Leu Leu Tyr Pro Leu Pro Gly Trp Val Leu Gly Asp
170                      100                     105                     110
171      Phe Met Cys Lys Phe Val Asn Tyr Ile Gln Gln Val Ser Val Gln Ala
172                      115                     120                     125
173      Thr Cys Ala Thr Leu Thr Ala Met Ser Val Asp Arg Trp Tyr Val Thr
174                      130                     135                     140
175      Val Phe Pro Leu Arg Ala Leu His Arg Arg Thr Pro Arg Leu Ala Leu
176      145                      150                      155                      160
177      Ala Val Ser Leu Ser Ile Trp Val Gly Ser Ala Ala Val Ser Ala Pro
178                      165                      170                      175
179      Val Leu Ala Leu His Arg Leu Ser Pro Gly Pro Arg Ala Tyr Cys Ser
180                      180                      185                      190
181      Glu Ala Phe Pro Ser Arg Ala Leu Glu Arg Ala Phe Ala Leu Tyr Asn
182                      195                      200                      205
183      Leu Leu Ala Leu Tyr Leu Leu Pro Leu Leu Ala Thr Cys Ala Cys Tyr
184      210                      215                      220
185      Ala Ala Met Leu Arg His Leu Gly Arg Val Ala Val Arg Pro Ala Pro
186      225                      230                      235                      240
187      Ala Asp Ser Ala Leu Gln Gly Gln Val Leu Ala Glu Arg Ala Gly Ala
188                      245                      250                      255
189      Val Arg Ala Lys Val Ser Arg Leu Val Ala Ala Val Val Leu Leu Phe
190                      260                      265                      270
191      Ala Ala Cys Trp Gly Pro Ile Gln Leu Phe Leu Val Leu Gln Ala Leu
192                      275                      280                      285
193      Gly Pro Ala Gly Ser Trp His Pro Arg Ser Tyr Ala Ala Tyr Ala Leu
194      290                      295                      300
195      Lys Thr Trp Ala His Cys Met Ser Tyr Ser Asn Ser Ala Leu Asn Pro
196      305                      310                      315                      320
197      Leu Leu Tyr Ala Phe Leu Gly Ser His Phe Arg Gln Ala Phe Arg Arg
198                      325                      330                      335
199      Val Cys Pro Cys Ala Pro Arg Arg Pro Arg Arg Pro Arg Pro Gly

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200          340          345          350
201 Pro Ser Asp Pro Ala Ala Pro His Ala Glu Leu His Arg Leu Gly Ser
202          355          360          365
203 His Pro Ala Pro Ala Arg Ala Gln Lys Pro Gly Ser Ser Gly Leu Ala
204          370          375          380
205 Ala Arg Gly Leu Cys Val Leu Gly Glu Asp Asn Ala Pro Leu
206          385          390          395
208 <210> SEQ ID NO: 10
209 <211> LENGTH: 1194
210 <212> TYPE: DNA
211 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 10
213 atgcacaccg tggctacgtc cggacccaac gcgtcctggg gggcaccggc caacgcctcc 60
214 ggctgcccgg gctgtggcgc caacgcctcg gacggcccag tcccttcgcc gcggggcgtg 120
215 gacgcctggc tegtgcctgt cttcttcgcg gcgctgatgc tgcctggcct ggtggggaac 180
216 tgcctgggta tctacgtcat ctgccgccac aagccgatgc ggaccgtgac caacttctac 240
217 atcgccaacc tggcggccac ggacgtgacc ttctctctgt gctgcgtccc cttcacggcc 300
218 ctgctgtacc cgtgcccgg ctgggtgctg ggcgacttca tgtgcaagtt cgtcaactac 360
219 atccagcagg tctcgggtga ggccacgtgt gccactctga ccgccatgag tgtggaccgc 420
220 tgggtacgtga cgggtgtccc gttgcgcgcc ctgcaccgcc gcacgccccg cctggcgtg 480
221 gctgtacgcc tcagcatctg ggtaggctct gcggcggtgt ctgcgcctgt gctcgccctg 540
222 caccgcctgt cacccgggcc gcgcgcctac tgcagtgagg ccttccccag ccgcgcctg 600
223 gacgcgcctt tgcactgta caacctgctg gcgctgtacc tgcctgcctg gctcgccacc 660
224 tgcgcctgct atgcggccat gctgcgccac ctgggcgggg tcgcctgctg ccccgcgccc 720
225 gccgatagcg cctgcagggg gcagggtgctg gcagagcgcg caggcgccgt gcggggccaa 780
226 gtctgcgggc tgggtggcgg cgtggtcctg ctcttcgccg cctgctgggg ccccatccag 840
227 ctgttcctgg tgcgcaggc gctgggcccc gcgggtcctt ggcacccaac cagctacgcc 900
228 gcctacgcgc ttaagacctg ggtcactgc atgtcctaca gcaactccgc gctgaacccg 960
229 ctgctctacg ccttctctgg ctcgcacttc cgacaggcct tcgcgcgctg tgcctcctgc 1020
230 gcgcgcgcgc gcccccgcgc cccccgcggg cccggacctt cggacccccc agccccacac 1080
231 gcggagctgc accgcctggg gtcccacccg gccccgcaca gggcgagaaa gccagggagc 1140
232 agtgggctgg ccgcgcgcgg gctgtgcgtc ctgggggagg acaacgcccc tctc 1194
234 <210> SEQ ID NO: 11
235 <211> LENGTH: 396
236 <212> TYPE: PRT
237 <213> ORGANISM: Rattus sp.
238 <400> SEQUENCE: 11
239 Met Ala Ala Glu Ala Thr Leu Gly Pro Asn Val Ser Trp Trp Ala Pro
240          5          10          15
241 Ser Asn Ala Ser Gly Cys Pro Gly Cys Gly Val Asn Ala Ser Asp Gly
242          20          25          30
243 Pro Gly Ser Ala Pro Arg Pro Leu Asp Ala Trp Leu Val Pro Leu Phe
244          35          40          45
245 Phe Ala Ala Leu Met Leu Leu Gly Leu Val Gly Asn Ser Leu Val Ile
246          50          55          60
247 Phe Val Ile Cys Arg His Lys His Met Gln Thr Val Thr Asn Phe Tyr
248          65          70          75          80
249 Ile Ala Asn Leu Ala Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val
250          85          90          95
```

RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:15; Line(s) 403

Seq#:16; Line(s) 413

Seq#:17; Line(s) 423

Seq#:18; Line(s) 433

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:15,16,17,18

VERIFICATION SUMMARY

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